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1600

RAW SEQUENCE LISTING

DATE: 09/18/2002

PATENT APPLICATION: US/09/555,115A

TIME: 15:59:03

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09182002\I555115A.raw

3 <110> APPLICANT: Bohach, Gregory I.  
 5 <120> TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS  
 7 <130> FILE REFERENCE: 12136.1USWO  
 9 <140> CURRENT APPLICATION NUMBER: US 09/555,115A  
 10 <141> CURRENT FILING DATE: 2000-08-01  
 12 <150> PRIOR APPLICATION NUMBER: PCT/US98/25107  
 13 <151> PRIOR FILING DATE: 1998-12-01  
 15 <150> PRIOR APPLICATION NUMBER: US 60/067,357  
 16 <151> PRIOR FILING DATE: 1997-12-02  
 18 <160> NUMBER OF SEQ ID NOS: 66  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 240  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Staphylococcus aureus  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: MISC\_FEATURE  
 29 <222> LOCATION: (240)..(240)  
 30 <223> OTHER INFORMATION: Xaa is unknown.  
 33 <400> SEQUENCE: 1

35	Glu	Ser	Gln	Pro	Asp	Pro	Thr	Pro	Asp	Glu	Leu	His	Lys	Ala	Ser	Lys
36	1			5						10					15	
39	Phe	Thr	Gly	Leu	Met	Glu	Asn	Met	Lys	Val	Leu	Tyr	Asp	Asp	His	Tyr
40				20						25					30	
43	Val	Ser	Ala	Thr	Lys	Val	Lys	Ser	Val	Asp	Lys	Phe	Leu	Ala	His	Asp
44				35						40					45	
47	Leu	Ile	Tyr	Asn	Ile	Ser	Asp	Lys	Lys	Leu	Lys	Asn	Tyr	Asp	Lys	Val
48				50						55					60	
51	Lys	Thr	Glu	Leu	Leu	Asn	Glu	Gly	Leu	Ala	Lys	Lys	Tyr	Lys	Asp	Glu
52	65					70					75					80
55	Val	Val	Asp	Val	Tyr	Gly	Ser	Asn	Tyr	Tyr	Val	Asn	Cys	Tyr	Phe	Ser
56						85					90				95	
59	Ser	Lys	Asp	Asn	Val	Gly	Lys	Val	Thr	Gly	Gly	Lys	Thr	Cys	Met	Tyr
60				100						105					110	
63	Gly	Gly	Ile	Thr	Lys	His	Glu	Gly	Asn	His	Phe	Asp	Asn	Gly	Asn	Leu
64				115						120					125	
67	Gln	Asn	Val	Leu	Ile	Arg	Val	Tyr	Glu	Asn	Lys	Arg	Asn	Thr	Ile	Ser
68				130						135					140	
71	Phe	Glu	Val	Gln	Thr	Asp	Lys	Lys	Ser	Val	Thr	Ala	Gln	Glu	Leu	Asp
72	145					150						155				160
75	Ile	Lys	Ala	Arg	Asn	Phe	Leu	Ile	Asn	Lys	Lys	Asn	Leu	Tyr	Glu	Phe
76						165						170			175	
79	Asn	Ser	Ser	Pro	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Glu	Asn	Asn

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80 180 185 190  
 83 Gly Asn Thr Phe Trp Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe  
 84 195 200 205  
 87 Asp Gln Ser Lys Tyr Leu Met Tyr Asn Asp Asn Lys Thr Val Asp  
 88 210 215 220  
 91 Ser Lys Ser Val Lys Ile Glu Val His Leu Thr Thr Lys Asn Gly Xaa  
 92 225 230 235 240  
 95 <210> SEQ ID NO: 2  
 96 <211> LENGTH: 240  
 97 <212> TYPE: PRT  
 98 <213> ORGANISM: Staphylococcus aureus  
 100 <220> FEATURE:  
 101 <221> NAME/KEY: MISC\_FEATURE  
 102 <222> LOCATION: (240)..(240)  
 103 <223> OTHER INFORMATION: Xaa is unknown.  
 106 <400> SEQUENCE: 2  
 108 Glu Ser Gln Pro Asp Pro Thr Pro Asp Glu Leu His Lys Ser Ser Glu  
 109 1 5 10 15  
 112 Phe Thr Gly Thr Met Gly Asn Met Lys Tyr Leu Tyr Asp Asp His Tyr  
 113 20 25 30  
 116 Val Ser Ala Thr Lys Val Met Ser Val Asp Lys Phe Leu Ala His Asp  
 117 35 40 45  
 120 Leu Ile Tyr Asn Ile Ser Asp Lys Lys Leu Lys Asn Tyr Asp Lys Val  
 121 50 55 60  
 124 Lys Thr Glu Leu Leu Asn Glu Asp Leu Ala Lys Lys Tyr Lys Asp Glu  
 125 65 70 75 80  
 128 Val Val Asp Val Tyr Gly Ser Asn Tyr Tyr Val Asn Cys Tyr Phe Ser  
 129 85 90 95  
 132 Ser Lys Asp Asn Val Gly Lys Val Thr Gly Gly Lys Thr Cys Met Tyr  
 133 100 105 110  
 136 Gly Gly Ile Thr Lys His Glu Gly Asn His Phe Asp Asn Gly Asn Leu  
 137 115 120 125  
 140 Gln Asn Val Leu Ile Arg Val Tyr Glu Asn Lys Arg Asn Thr Ile Ser  
 141 130 135 140  
 144 Phe Glu Val Gln Thr Asp Lys Lys Ser Val Thr Ala Gln Glu Leu Asp  
 145 145 150 155 160  
 148 Ile Lys Ala Arg Asn Phe Leu Ile Asn Lys Lys Asn Leu Tyr Glu Phe  
 149 165 170 175  
 152 Asn Ser Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Asn Asn  
 153 180 185 190  
 156 Gly Asn Thr Phe Gln Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe  
 157 195 200 205  
 160 Asp Gln Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn Lys Thr Val Asp  
 161 210 215 220  
 164 Ser Lys Ser Val Lys Ile Glu Val His Leu Thr Thr Lys Asn Gly Xaa  
 165 225 230 235 240  
 168 <210> SEQ ID NO: 3  
 169 <211> LENGTH: 240  
 170 <212> TYPE: PRT

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171 <213> ORGANISM: Staphylococcus aureus
173 <220> FEATURE:
174 <221> NAME/KEY: MISC_FEATURE
175 <222> LOCATION: (240)..(240)
176 <223> OTHER INFORMATION: Xaa is unknown.
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185 Phe Thr Gly Thr Met Gly Asn Met Lys Tyr Leu Tyr Asp Asp His Tyr
186 20 25 30
189 Val Ser Ala Thr Lys Val Lys Ser Val Asp Lys Phe Leu Ala His Asp
190 35 40 45
193 Leu Ile Tyr Asn Ile Ser Asp Lys Lys Leu Lys Asn Tyr Asp Lys Val
194 50 55 60
197 Lys Thr Glu Leu Leu Asn Glu Asp Leu Ala Lys Lys Tyr Lys Asp Glu
198 65 70 75 80
201 Val Val Asp Val Tyr Gly Ser Asn Tyr Tyr Val Asn Cys Tyr Phe Ser
202 85 90 95
205 Ser Lys Asp Asn Val Gly Lys Val Thr Gly Gly Lys Thr Cys Met Tyr
206 100 105 110
209 Gly Gly Ile Thr Lys His Glu Gly Asn His Phe Asp Asn Gly Asn Leu
210 115 120 125
213 Gln Asn Val Leu Val Arg Val Tyr Glu Asn Lys Arg Asn Thr Ile Ser
214 130 135 140
217 Phe Glu Val Gln Thr Asp Lys Lys Ser Val Thr Ala Gln Glu Leu Asp
218 145 150 155 160
221 Ile Lys Ala Arg Asn Phe Leu Ile Asn Lys Lys Asn Leu Tyr Glu Phe
222 165 170 175
225 Asn Ser Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Asn Asn
226 180 185 190
229 Gly Asn Thr Phe Gln Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe
230 195 200 205
233 Asp Gln Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn Lys Thr Val Asp
234 210 215 220
237 Ser Lys Ser Val Lys Ile Glu Val His Leu Thr Thr Lys Asn Gly Xaa
238 225 230 235 240
241 <210> SEQ ID NO: 4
242 <211> LENGTH: 240
243 <212> TYPE: PRT
244 <213> ORGANISM: Staphylococcus aureus
246 <220> FEATURE:
247 <221> NAME/KEY: MISC_FEATURE
248 <222> LOCATION: (240)..(240)
249 <223> OTHER INFORMATION: Xaa is unknown.
252 <400> SEQUENCE: 4
254 Glu Ser Gln Pro Asp Pro Met Pro Asp Asp Leu His Lys Ser Ser Glu
255 1 5 10 15
258 Phe Thr Gly Thr Met Gly Asn Met Lys Tyr Leu Tyr Asp Asp His Tyr
259 20 25 30

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TIME: 15:59:03

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09182002\I555115A.raw

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262 Val Ser Ala Thr Lys Val Lys Ser Val Asp Lys Phe Leu Ala His Asp
263          35          40          45
266 Leu Ile Tyr Asn Ile Asn Asp Lys Lys Leu Asn Asn Tyr Asp Lys Val
267          50          55          60
270 Lys Thr Glu Leu Leu Asn Glu Asp Leu Ala Asn Lys Tyr Lys Asp Glu
271 65          70          75          80
274 Val Val Asp Val Tyr Gly Ser Asn Tyr Tyr Val Asn Cys Tyr Phe Ser
275          85          90          95
278 Ser Lys Asp Asn Val Gly Lys Val Thr Ser Gly Lys Thr Cys Met Tyr
279          100          105          110
282 Gly Gly Ile Thr Lys His Glu Gly Asn His Phe Asp Asn Gly Asn Leu
283          115          120          125
286 Gln Asn Val Leu Ile Arg Val Tyr Glu Asn Lys Arg Asn Thr Ile Ser
287          130          135          140
290 Phe Glu Val Gln Thr Asp Lys Lys Ser Val Thr Ala Gln Glu Leu Asp
291 145          150          155          160
294 Ile Lys Ala Arg Asn Phe Leu Ile Asn Lys Lys Asn Leu Tyr Glu Phe
295          165          170          175
298 Asn Ser Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Ser Asn
299          180          185          190
302 Gly Asn Thr Phe Trp Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe
303          195          200          205
306 Asp Gln Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Lys Met Val Asp
307          210          215          220
310 Ser Lys Ser Val Lys Ile Glu Val His Leu Thr Thr Lys Asn Gly Xaa
311 225          230          235          240
314 <210> SEQ ID NO: 5
315 <211> LENGTH: 240
316 <212> TYPE: PRT
317 <213> ORGANISM: Staphylococcus aureus
319 <220> FEATURE:
320 <221> NAME/KEY: MISC_FEATURE
321 <222> LOCATION: (240)..(240)
322 <223> OTHER INFORMATION: Xaa is unknown.
325 <400> SEQUENCE: 5
327 Glu Ser Gln Pro Asp Pro Thr Pro Asp Glu Leu His Lys Ser Ser Glu
328 1          5          10          15
331 Phe Thr Gly Thr Met Gly Asn Met Lys Tyr Leu Tyr Asp Asp His Tyr
332          20          25          30
335 Val Ser Ala Thr Lys Val Lys Ser Val Asp Lys Phe Leu Ala His Asp
336          35          40          45
339 Leu Ile Tyr Asn Ile Ser Asp Lys Lys Leu Lys Asn Tyr Asp Lys Val
340          50          55          60
343 Lys Thr Glu Leu Leu Asn Glu Asp Leu Ala Lys Lys Tyr Lys Asp Glu
344 65          70          75          80
347 Val Val Asp Val Tyr Gly Ser Asn Tyr Tyr Val Asn Cys Tyr Phe Ser
348          85          90          95
351 Ser Lys Asp Asn Val Gly Lys Val Thr Gly Gly Lys Thr Cys Met Tyr
352          100          105          110

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TIME: 15:59:03

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355 Gly Gly Ile Thr Lys His Glu Gly Asn His Phe Asp Asn Gly Asn Leu
356      115      120      125
359 Gln Asn Val Leu Ile Arg Val Tyr Glu Asn Lys Arg Asn Thr Ile Ser
360      130      135      140
363 Phe Glu Val Gln Thr Asp Lys Lys Ser Val Thr Ala Gln Glu Leu Asp
364 145      150      155      160
367 Ile Lys Ala Arg Asn Phe Leu Ile Asn Lys Lys Asn Leu Tyr Glu Phe
368      165      170      175
371 Asn Ser Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Asn Asn
372      180      185      190
375 Gly Asn Thr Phe Gln Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe
376      195      200      205
379 Asp Gln Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn Lys Thr Val Asp
380      210      215      220
383 Ser Lys Arg Val Lys Ile Glu Val His Leu Thr Thr Lys Asn Gly Xaa
384 225      230      235      240
387 <210> SEQ ID NO: 6
388 <211> LENGTH: 240
389 <212> TYPE: PRT
390 <213> ORGANISM: Staphylococcus aureus
392 <220> FEATURE:
393 <221> NAME/KEY: MISC_FEATURE
394 <222> LOCATION: (240)..(240)
395 <223> OTHER INFORMATION: Xaa is unknown.
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400 Glu Ser Gln Pro Asp Pro Met Pro Asp Asp Leu His Lys Ser Ser Glu
401 1      5      10      15
404 Phe Thr Gly Thr Met Gly Asn Met Lys Tyr Leu Tyr Asp Asp His Tyr
405      20      25      30
408 Val Ser Ala Thr Lys Val Lys Ser Val Asp Lys Phe Leu Ala His Asp
409      35      40      45
412 Leu Ile Tyr Asn Ile Ser Asp Lys Arg Leu Lys Asn Tyr Asp Lys Val
413      50      55      60
416 Lys Thr Glu Leu Leu Asn Glu Asp Leu Ala Lys Lys Tyr Lys Asp Glu
417 65      70      75      80
420 Val Val Asp Val Tyr Gly Ser Asn Tyr Tyr Val Asn Cys Tyr Phe Ser
421      85      90      95
424 Ser Lys Asp Asn Val Gly Lys Val Thr Gly Gly Lys Thr Cys Met Tyr
425      100      105      110
428 Gly Gly Ile Thr Lys His Glu Gly Asn His Phe Asp Asn Gly Asn Leu
429      115      120      125
432 Gln Asn Val Leu Val Arg Val Tyr Glu Asn Lys Arg Asn Thr Ile Ser
433      130      135      140
436 Phe Glu Val Gln Thr Asp Lys Lys Ser Val Thr Ala Gln Glu Leu Asp
437 145      150      155      160
440 Ile Lys Ala Arg Asn Phe Leu Ile Asn Lys Lys Asn Leu Tyr Glu Phe
441      165      170      175
444 Asn Ser Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Asn Asn
445      180      185      190

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/18/2002  
PATENT APPLICATION: US/09/555,115A      TIME: 15:59:04

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF4\09182002\I555115A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 240  
Seq#:2; Xaa Pos. 240  
Seq#:3; Xaa Pos. 240  
Seq#:4; Xaa Pos. 240  
Seq#:5; Xaa Pos. 240  
Seq#:6; Xaa Pos. 240  
Seq#:7; Xaa Pos. 240  
Seq#:8; Xaa Pos. 240